

Amendments to the Specification

Please replace the table beginning on page 12, line 11, of the specification with the following amended table:

Genetic variation type	Uniform resource location
SNP	http://bioinfo.pal.roche.com/usuka_bioinformatics/cgi-bin/msnp/msnp.pl <u>bioinfo.pal.roche.com/usuka_bioinformatics/cgi-bin/msnp/msnp.pl</u>
SNP	http://snp.cshl.org/ <u>snp.cshl.org/</u>
SNP	http://www.ibc.wustl.edu/SNP/ <u>www.ibc.wustl.edu/SNP/</u>
SNP	http://www-genome.wi.mit.edu/SNP/mouse/ <u>www-genome.wi.mit.edu/SNP/mouse/</u>
SNP	http://www.ncbi.nlm.nih.gov/SNP/ <u>www.ncbi.nlm.nih.gov/SNP/</u>
Microsatellite markers	http://www.informatics.jax.org/searches/polymorphism_form.shtml <u>www.informatics.jax.org/searches/polymorphism_form.shtml</u>
Restriction fragment length polymorphisms	http://www.informatics.jax.org/searches/polymorphism_form.shtml <u>www.informatics.jax.org/searches/polymorphism_form.shtml</u>
Short tandem repeats	http://www.cidr.jhmi.edu/mouse/mmset.html <u>www.cidr.jhmi.edu/mouse/mmset.html</u>
Sequence length polymorphisms	http://mebio.med.buffalo.edu/mit.html <u>mcbio.med.buffalo.edu/mit.html</u>
DNA methylation database	http://genome.imb-jena.de/public.html <u>genome.imb-jena.de/public.html</u>

Please replace the paragraph beginning on page 12, line 14, of the specification with the following amended paragraph:

In addition, the genetic variations used by the methods of the present invention may involve differences in the expression levels of genes rather than actual identified variations in the composition of the genome of the organism of interest. Therefore, genotypic databases 52 within the scope of the present invention include a wide array of expression profile databases such as the one found at the URL:

~~<http://www.ncbi.nlm.nih.gov/geo/>~~
www.ncbi.nlm.nih.gov/geo/

It will be appreciated that when the variation tracked by genotypic database 52 is a variation in the expression level of a gene rather than a variation in the genome, there is no requirement that genomic database 52 be populated with elements such as locus 54.

Please replace the paragraph beginning on page 22, line 27, of the specification with the following amended paragraph:

In some embodiments of the present invention, two locus positions L^1 and L^2 in locus L are considered to be in the same gene if both positions map to a region of DNA that has been assigned the same accession number in a genetic database. Genetic databases include databases such as the Human Genome Database (GDB), Saccharomyces Genome Database (SGD), Mouse Genome Database (MGD), Drosophila Genetic Database (FLYBASE IMGT/LIGM) ~~http://www.ebi.ac.uk/embl/Documentation/User_manual/dr_line.html~~ (www.ebi.ac.uk/embl/Documentation/User_manual/dr_line.html) or Genbank (~~<http://www.ncbi.nlm.nih.gov/Genbank/>~~) (www.ncbi.nlm.nih.gov/Genbank/). Many other genetic databases are known and are within the scope of the present invention.